

FIRST APPROXIMATION TO THE STUDY OF THE PROTEOME OF MESOAMERICAN AND ANDEAN BEAN GENOTYPES

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Proteomics has made it possible to identify a broad spectrum of proteins in different species. It is expected to revolutionize plant research, because it offers researchers new opportunities to increase the knowledge about both plant biology and crops improvement. This is unique technique not only for its ability to simultaneously separate thousand of proteins but also for detecting post-and co-translational modifications, which cannot be predicted from genome sequences. *Phaseolus vulgaris* has been suggested to be a model species to be investigated due to its selfish and synteny with respect to other legume species (Gepts et al. 2005). This situation points at bean as a good model to be analysed by proteomic methodology. This is the reason why we are initiating an approach to bean proteomics by two-dimensional electrophoresis (2-DE) with immobilized pH gradients (IPGs). One of the critical problems that researchers have to take into account, when working in proteomics, is the low amount of proteins and the presence of some compound that can be interacting with proteomic protocols (Rose et al. 2004). In order to overcome these problems and go into the knowledge of bean extractome, it is necessary to establish which protocols of extraction are rendering the best results. With this purpose, leaves and seeds from two varieties representatives of both originary pools, Mesoamerican and Andean, are being analysed. Three different protocols of extraction are being used in both tissues and samples: TCA-acetone, Phenol and a commercial extraction kit (Clean-up Kit). The results show that there are appropriate protocols for each tissue of *Phaseolus vulgaris*.

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References

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